

## SEQUENCE LISTING

<110> Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of  
Flavivirus Infection

<130> 14114.0332U3

<150> PCT/US99/12298

<151> 1999-06-03

<150> 09/701,536

<151> 2000-11-29

<150> 60/087,908

<151> 1998-06-04

<160> 31

<170> FastSEQ for Windows Version 4.0

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<211> 48

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&lt;223&gt; Amplimer YFDV389

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48

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&lt;210&gt; 5

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&lt;212&gt; DNA

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ttctctgttg	agatccagtt	cgatgtaac	cactcgtgca	cccaactgat	cttcagcata	7269
accagcgttt	accagcgctt	cggtgtgagc	aaaaacagga	aggcaaatat	ccgcaaaaaa	7329
gggaataaag	gcgcacagga	aatgttgaa	actcatactc	ttcttttttc	aatattatgt	7389
aagcattatc	cagggttatt	gtctcatatg	cggtatcata	tttgaagtat	tttagaaaaa	7449
taaaacaata	aaatttccac	gcacattctc	cccaaaagct	ccaactcagc	t	7509

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<210> 11
<211> 697
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of artificial sequence; note =  
synthetic construct

&lt;223&gt; pCDJE 2-7

<400> 11  
 Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met  
 1 5 10 15  
 Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys  
 20 25 30  
 Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp  
 35 40 45  
 Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys  
 50 55 60  
 Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr  
 65 70 75 80  
 Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp  
 85 90 95  
 Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr  
 100 105 110  
 Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr  
 115 120 125  
 His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser  
 130 135 140  
 Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg  
 145 150 155 160  
 Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly  
 165 170 175  
 Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val  
 180 185 190  
 Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe  
 195 200 205  
 Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly  
 210 215 220  
 Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val  
 225 230 235 240  
 Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr  
 245 250 255  
 Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro  
 260 265 270  
 Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val  
 275 280 285  
 Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu  
 290 295 300  
 Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser  
 305 310 315 320  
 Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val  
 325 330 335  
 Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr  
 340 345 350  
 Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro  
 355 360 365  
 Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr  
 370 375 380  
 Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val  
 385 390 395 400  
 Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His  
 405 410 415

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Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn  
                   420                  425                  430  
 Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser  
                   435                  440                  445  
 Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala  
                   450                  455                  460  
 Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly  
                   465                  470                  475                  480  
 His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr  
                   485                  490                  495  
 Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala  
                   500                  505                  510  
 Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser  
                   515                  520                  525  
 Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp  
                   530                  535                  540  
 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr  
                   545                  550                  555                  560  
 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly  
                   565                  570                  575  
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His  
                   580                  585                  590  
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu  
                   595                  600                  605  
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe  
                   610                  615                  620  
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln  
                   625                  630                  635                  640  
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile  
                   645                  650                  655  
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala  
                   660                  665                  670  
 Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu  
                   675                  680                  685  
 Val Phe Leu Ala Thr Asn Val His Ala  
                   690                  695

&lt;210&gt; 12

&lt;211&gt; 46

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of artificial sequence; note =  
       synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; 1-46

&lt;223&gt; WN 466

&lt;400&gt; 12

cttggtagcc gtctcgccgc cgtgaccctc tcgaacttcc agggca

<210> 13  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<221> misc\_feature  
 <222> 1-43  
 <223> CWN2444

<400> 13  
 agaggcactt gcacgtgcgg attccgccg gcgaaaaaga aaa

43

<210> 14  
 <211> 24  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<223> JB Signal

<400> 14  
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
 1 5 10 15  
 Val Val Ile Ala Cys Ala Gly Ala  
 20

<210> 15  
 <211> 5308  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<221> CDS  
 <222> (911)...(2987)

<221> misc\_feature  
 <222> (1)...(5308)  
 <223> pCBWN

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 cgcataatgt aagccagtat ctgctccctg cttgtgtgtt ggaggctcgt gagtagtgcg 120  
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

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tggagtccgc	cggttacataa	cttacggtaa	atggcccgcc	tggctgacgc	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
attgacgtca	atgggtggag	tatttacggt	aaactgccca	cttggcgagta	catcaaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaattggccc	gcctggcatt	540
atgcccgata	catgacctta	tgggactttc	ctacttgga	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggtttttgg	cagtacatca	atgggcgtgg	atagcggttt	660
gactcaagg	gatttccaag	tctccacccc	attgacgtca	atgggagttt	gttttggcac	720
caaaatcaac	gggactttcc	aaaatgtcgt	aacaactccg	ccccattgac	gcaaatgggc	780
ggtaggcgtg	tacgggtggga	ggtctatata	agcagagctc	tctggctaac	tagagaaccc	840
actgcttact	ggcttatcga	aattaatacg	actcaetata	gggagaccca	agcttggtac	900
cgccgcgcgc	atg ggc aag agg tcc gcc ggc	tca atc atg tgg ctc gcg				949
	Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala					
	1	5		10		

agc	ttg	gca	gtt	gtc	ata	gct	tgt	gca	ggc	gcc	gtg	acc	ctc	tcg	aac	997
Ser	Leu	Ala	Val	Val	Ile	Ala	Cys	Ala	Gly	Ala	Val	Thr	Leu	Ser	Asn	
	15					20						25				

ttc	cag	ggc	aag	gtg	atg	atg	acg	gta	aat	gct	act	gac	gtc	aca	gat	1045
Phe	Gln	Gly	Lys	Val	Met	Met	Thr	Val	Asn	Ala	Thr	Asp	Val	Thr	Asp	
	30				35					40					45	

gtc	atc	acg	att	cca	aca	gct	gct	gga	aag	aac	cta	tgc	att	gtc	aga	1093
Val	Ile	Thr	Ile	Pro	Thr	Ala	Ala	Gly	Lys	Asn	Leu	Cys	Ile	Val	Arg	
				50					55					60		

gca	atg	gat	gtg	gga	tac	atg	tgc	gat	gat	act	act	act	tat	gaa	tgc	1141
Ala	Met	Asp	Val	Gly	Tyr	Met	Cys	Asp	Asp	Thr	Ile	Thr	Tyr	Glu	Cys	
		65						70					75			

cca	gtg	ctg	tcg	gct	ggc	aat	gat	cca	gaa	gac	atc	gac	tgt	tgg	tgc	1189
Pro	Val	Leu	Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	
		80				85							90			

aca	aag	tca	gca	gtc	tac	gtc	agg	tat	gga	aga	tgc	acc	aag	aca	cgc	1237
Thr	Lys	Ser	Ala	Val	Tyr	Val	Arg	Tyr	Gly	Arg	Cys	Thr	Lys	Thr	Arg	
	95					100					105					

cac	tca	aga	cgc	agt	cgg	agg	tca	ctg	aca	gtg	cag	aca	cac	gga	gaa	1285
His	Ser	Arg	Arg	Ser	Arg	Arg	Ser	Leu	Thr	Val	Gln	Thr	His	Gly	Glu	
	110				115					120				125		

agc	act	cta	gcg	aac	aag	aag	ggg	gct	tgg	atg	gac	agc	acc	aag	gcc	1333
Ser	Thr	Leu	Ala	Asn	Lys	Lys	Gly	Ala	Trp	Met	Asp	Ser	Thr	Lys	Ala	
			130						135					140		

aca	agg	tat	ttg	gta	aaa	aca	gaa	tca	tgg	atc	ttg	agg	aac	cct	gga	1381
Thr	Arg	Tyr	Leu	Val	Lys	Thr	Glu	Ser	Trp	Ile	Leu	Arg	Asn	Pro	Gly	
			145				150							155		

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tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc 1429  
 Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr  
 160 165 170

atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct 1477  
 Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala  
 175 180 185

tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga 1525  
 Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly  
 190 195 200 205

gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc 1573  
 Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys  
 210 215 220

gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg 1621  
 Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met  
 225 230 235

aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg 1669  
 Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu  
 240 245 250

gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga 1717  
 Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly  
 255 260 265

gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa 1765  
 Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln  
 270 275 280 285

gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa 1813  
 Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys  
 290 295 300

gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata 1861  
 Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile  
 305 310 315

gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt 1909  
 Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe  
 320 325 330

gtc cat gga cca act act gtg gag tgc cac gga aac tac tcc aca cag 1957  
 Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln  
 335 340 345

gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct 2005  
 Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro  
 350 355 360 365

tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt 2053

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Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys	
370 375 380	
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt	2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val	
385 390 395	
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac	2149
Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn	
400 405 410	
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg	2197
Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr	
415 420 425	
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca	2245
Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala	
430 435 440 445	
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att	2293
Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile	
450 455 460	
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tog ggt cat ttg	2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu	
465 470 475	
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat	2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr	
480 485 490	
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca	2437
Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr	
495 500 505	
ggc cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga	2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly	
510 515 520 525	
cct tgc aaa gtt cct atc tgc tca gtg gct tca ttg aac gac cta acg	2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr	
530 535 540	
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg	2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr	
545 550 555	
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca	2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser	
560 565 570	
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac	2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His	
575 580 585	





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gaagtgtgtcc  tgcgaacttta  tccgcctcca  tccagtcctat  taattgtgtgc  cgggaagcta  4577
gagtaagtag  ttcgccagttt  aatagtttgc  gcaacggtgt  tgcattgtct  acaggcatcg  4637
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tcctttttca  atattattga  agcattttat  aggggttatg  tctcatgagc  ggatacatat  5237
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&lt;210&gt; 16

&lt;211&gt; 692

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;223&gt; pCBWN

&lt;400&gt; 16

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
 20          25          30
Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
 35          40          45
Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
 50          55          60
Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
 65          70          75          80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
 85          90          95
Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
100          105          110
Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
115          120          125
Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
130          135          140
Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145          150          155          160
Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
165          170          175
Val Val Phe Val Val Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
180          185          190
Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
195          200          205

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00000116 041010

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile  
 210 215 220  
 Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu  
 225 230 235 240  
 Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val  
 245 250 255  
 Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His  
 260 265 270  
 Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val  
 275 280 285  
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile  
 290 295 300  
 Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr  
 305 310 315 320  
 Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly  
 325 330 335  
 Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala  
 340 345 350  
 Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr  
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 Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg  
 370 375 380  
 Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys  
 385 390 395 400  
 Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp  
 405 410 415  
 Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu  
 420 425 430  
 Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser  
 435 440 445  
 Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu  
 450 455 460  
 Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg  
 465 470 475 480  
 Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys  
 485 490 495  
 Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly  
 500 505 510  
 Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys  
 515 520 525  
 Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly  
 530 535 540  
 Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala  
 545 550 555 560  
 Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 565 570 575  
 Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly  
 580 585 590  
 Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg  
 595 600 605  
 Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly  
 610 615 620  
 Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 625 630 635 640

10-40-40 5-11-50-50

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
                   645                  650                  655  
 Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile  
                   660                  665                  670  
 Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val  
                   675                  680                  685  
 Asn Val His Ala  
                   690

<210> 17  
 <211> 5334  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
       synthetic construct

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 <222> (916)...(3007)  
 <221> misc\_feature  
 <222> (1)...(5334)  
 <223> pCBUE 1-14

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 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180  
 ttagggttag cggttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240  
 gattattgac tagttattaa tagtaaatcaa ttacggggctc attagttcat agcccatata 300  
 tggagtcccg cgttacataa cttacggtaa atggcccgcc tggttgaccg cccaacgacc 360  
 cccgccattt gacgtcaata atgacgtatg ttcccatagt aacgcacaata gggactttcc 420  
 attgacgtca atgggtggag tattttacggt aaactgccca cttggcagta catcaagtgc 480  
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<223> Description of artificial sequence; note =  
synthetic construct

<223> pCBUE 1-14

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&lt;400&gt; 18

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Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys	
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Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly	
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His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro	
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Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn	
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Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
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ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct    1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala
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Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro
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gtc gaa gag gtg tgg gtc cac tac ggc aga tgc acg cgc atg gga cat    1239
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tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc    1287

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Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr	
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Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr	
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Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val	
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Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu	
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Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val	
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Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala	
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&lt;210&gt; 22

&lt;211&gt; 692

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;400&gt; 22

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Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
          35           40           45
Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
          50           55           60
Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
          65           70           75           80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
          85           90           95
Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
          100          105          110
Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
          115          120          125
Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
          130          135          140

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Val	Ala	Leu	Ala	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Asn	Thr	Gln	Arg
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Val	Val	Phe	Val	Ile	Met	Leu	Met	Leu	Ile	Ala	Pro	Ala	Tyr	Ser	Phe
			180					185					190		
Asn	Cys	Leu	Gly	Thr	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Ala	Ser	Gly
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Ala	Thr	Trp	Ile	Asp	Leu	Val	Leu	Glu	Gly	Gly	Ser	Cys	Val	Thr	Val
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Met	Ala	Pro	Glu	Lys	Pro	Thr	Leu	Asp	Phe	Lys	Val	Met	Lys	Met	Glu
225					230					235					240
Ala	Thr	Glu	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Cys	Tyr	Glu	Ala	Thr	Leu
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Asp	Thr	Leu	Ser	Thr	Val	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His
		260						265					270		
Asn	Thr	Lys	Arg	Ser	Asp	Pro	Thr	Phe	Val	Cys	Lys	Arg	Asp	Val	Val
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Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile
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Asp	Thr	Cys	Ala	Lys	Phe	Thr	Cys	Lys	Asn	Lys	Ala	Thr	Gly	Lys	Thr
305					310					315					320
Ile	Leu	Arg	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val	His	Gly
			325						330					335	
Ser	Thr	Asp	Ser	Thr	Ser	His	Gly	Asn	Tyr	Ser	Glu	Gln	Ile	Gly	Lys
		340						345					350		
Asn	Gln	Ala	Ala	Arg	Phe	Thr	Ile	Ser	Pro	Gln	Ala	Pro	Ser	Phe	Thr
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Ala	Asn	Met	Gly	Glu	Tyr	Gly	Thr	Val	Thr	Ile	Asp	Cys	Glu	Ala	Arg
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Ser	Gly	Ile	Asn	Thr	Glu	Asp	Tyr	Tyr	Val	Phe	Thr	Val	Lys	Glu	Lys
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Ser	Trp	Leu	Val	Asn	Arg	Asp	Trp	Phe	His	Asp	Leu	Asn	Leu	Pro	Trp
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Thr	Ser	Pro	Ala	Thr	Thr	Asp	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Val	Glu
			420					425					430		
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Thr	Val	Val	Ala	Leu	Gly	Ser
		435					440					445			
Gln	Glu	Gly	Ala	Leu	His	Thr	Ala	Leu	Ala	Gly	Ala	Ile	Pro	Ala	Thr
	450					455					460				
Val	Ser	Ser	Ser	Thr	Leu	Thr	Leu	Gln	Ser	Gly	His	Leu	Lys	Cys	Arg
465					470					475					480
Ala	Lys	Leu	Asp	Lys	Val	Lys	Ile	Lys	Gly	Thr	Thr	Tyr	Gly	Met	Cys
			485						490					495	
Asp	Ser														

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly  
 580 585 590  
 Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg  
 595 600 605  
 Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
 610 615 620  
 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 625 630 635 640  
 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
 645 650 655  
 Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile  
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 Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr  
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 Ser Val Gln Ala  
 690

<210> 23  
 <211> 5271  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

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 <222> (910)...(2953)

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 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180  
 ttagggttag gcgttttgcg ctgccttcgag atgtacgggc cagatatacg cgttgacatt 240  
 gattattgac tagttattaa tagtaataca ttacggggctc attagttcat agcccatata 300  
 tggagtcccg cgttacataa cttacggtga atggcccgcg tggctgacgc cccaacgacc 360  
 cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420  
 attgacgtca atgggtggac tatttacggt aaactgccca cttggcgagta catcaagtgt 480  
 atcatatgcc aagtagcgc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540  
 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600  
 tcgctattac catggtgatg cgggttttggc agtacaatca tgggcgtgga tagcgggttg 660  
 actcacgggg atttccaagt ctccaccoca ttgacgtcaa tggggagtgtg ttttggcacc 720  
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatggcgcc 780  
 gtaggcgtgt acggtgggag gtctatatata gcagagctct ctggctaact agagaaccga 840  
 ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccocaa gcttgggtacc 900  
 gccgcgcccg atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951  
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser  
 1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999  
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys  
 15 20 25 30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047

Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr  
 35 40 45

ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag 1095  
 Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys  
 50 55 60

tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca 1143  
 Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro  
 65 70 75

aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac 1191  
 Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn  
 80 85 90

gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg 1239  
 Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg  
 95 100 105 110

tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag 1287  
 Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys  
 115 120 125

acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc 1335  
 Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu  
 130 135 140

caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg 1383  
 Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr  
 145 150 155

gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc 1431  
 Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val  
 160 165 170

gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac 1479  
 Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His  
 175 180 185 190

tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga 1527  
 Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly  
 195 200 205

act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg 1575  
 Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met  
 210 215 220

gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att 1623  
 Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile  
 225 230 235

gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act 1671  
 Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr  
 240 245 250

2025-11-13 14:33:33

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gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp 275 280 285	1767
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val 290 295 300	1815
gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val 305 310 315	1863
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly 320 325 330	1911
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp 335 340 345 350	1959
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala 355 360 365	2007
aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr 370 375 380	2055
atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala 385 390 395	2103
cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg 400 405 410	2151
gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile 415 420 425 430	2199
aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu 435 440 445	2247
act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr 450 455 460	2295
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ORIGINAL SUBMITTED



Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu  
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aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt 2391  
 Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe  
 480 485 490

gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg 2439  
 Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val  
 495 500 505 510

aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat 2487  
 Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp  
 515 520 525

gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc 2535  
 Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro  
 530 535 540

atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct 2583  
 Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro  
 545 550 555

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 Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr  
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tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag 2679  
 Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln  
 575 580 585 590

acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg 2727  
 Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp  
 595 600 605

gat ttc agc tcc gct gga ggg ttc ttc act tgc gtt ggg aaa gga att 2775  
 Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile  
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cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac 2823  
 His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn  
 625 630 635

tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc 2871  
 Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile  
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 655 660 665 670

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 Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala  
 675 680

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&lt;210&gt; 24

&lt;211&gt; 681

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;400&gt; 24

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1

5

10

15

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 Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser  
 35 40 45  
 Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp  
 50 55 60  
 Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu  
 65 70 75 80  
 Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg  
 85 90 95  
 Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg  
 100 105 110  
 Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg  
 115 120 125  
 Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys  
 130 135 140  
 Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu  
 145 150 155 160  
 Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile  
 165 170 175  
 Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile  
 180 185 190  
 Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp  
 195 200 205  
 Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro  
 210 215 220  
 Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg  
 225 230 235 240  
 Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val  
 245 250 255  
 Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu  
 260 265 270  
 Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly  
 275 280 285  
 Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys  
 290 295 300  
 Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln  
 305 310 315 320  
 Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys  
 325 330 335  
 Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu  
 340 345 350  
 Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu  
 355 360 365  
 Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala  
 370 375 380  
 Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp  
 385 390 395 400  
 Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met  
 405 410 415  
 His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val  
 420 425 430  
 Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly  
 435 440 445

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Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
  450                      455                      460
His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
  465                      470                      475                      480
Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
                      485                      490                      495
Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
  500                      505                      510
Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
  515                      520                      525
Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
  530                      535                      540
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
  545                      550                      555                      560
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
                      565                      570                      575
Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
  580                      585                      590
Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
  595                      600                      605
Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
  610                      615                      620
Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
  625                      630                      635                      640
Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
                      645                      650                      655
Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
  660                      665                      670
Met Phe Leu Ser Leu Gly Val Gly Ala
  675                      680

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&lt;210&gt; 25

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of artificial sequence; note =  
synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; 1-35

&lt;223&gt; POW 454

&lt;400&gt; 25

aaaagaaaaa gcgctaccac catccaccgg gacag

35

&lt;210&gt; 26

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
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<221> misc\_feature

<222> 1-41

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41

<210> 27

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<223> Modified JE Signal

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala

1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala

20

<210> 28

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<212> DNA

<213> Artificial Sequence

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<221> misc\_feature

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36

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<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of artificial sequence; note =  
synthetic construct

41

41

40